

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: SMITH, Craig A.
GOODWIN, Raymond G.
BECKMANN, M. Patricia
- (ii) TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS
FACTOR- α AND - β RECEPTORS
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: IMMUNEX CORPORATION
 - (B) STREET: 51 University Street
 - (C) CITY: Seattle
 - (D) STATE: WASHINGTON
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 98101
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/144,502
 - (B) FILING DATE: 31-AUG-1998
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/346,555
 - (B) FILING DATE: 29-NOV-1994
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 07/523,635
 - (B) FILING DATE: 10-MAY-1990
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 07/421,417
 - (B) FILING DATE: 13-OCT-1989
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 07/405,370
 - (B) FILING DATE: 11-SEPT-1989
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 07/403,241
 - (B) FILING DATE: 05-SEPT-1989

(viii) ATTORNEY/AGENT INFORMATION:
 (A) NAME: KIT, Gordon
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 (C) REFERENCE/DOCKET NUMBER: A-7210

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1641 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
 (G) CELL TYPE: Fibroblast
 (H) CELL LINE: WI-26 VA4

(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: WI-26 VA4
 (B) CLONE: 1

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 88..1473

(ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 154..1470

(ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 88..153

(x) PUBLICATION INFORMATION:
 (A) AUTHORS: Smith, Craig A.
 Davis, Terri
 Anderson, Dirk
 Solam, Lisabeth
 Beckmann, M. P.
 Jerzy, Rita
 Dower, Steven K.
 Cosman, David
 Goodwin, Raymond G.

(B) TITLE: A Receptor for Tumor Necrosis
Factor Defines an Unusual Family
of Cellular and Viral Proteins

(C) JOURNAL: Science

(D) VOLUME: 248

(F) PAGES: 1019-1023

(G) DATE: 25-MAY-1990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCGAGGCAGG CAGCCTGGAG AGAAGGCGCT GGGCTGCGAG GGCGCGAGGG CGCGAGGGCA	60
GGGGGCAACC GGACCCCGCC CGCATCC ATG GCG CCC GTC GCC GTC TGG GCC	111
Met Ala Pro Val Ala Val Trp Ala	
-22 -20 -15	
GCG CTG GCC GTC GGA CTG GAG CTC TGG GCT GCG GCG CAC GCC TTG CCC	159
Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala Ala His Ala Leu Pro	
-10 -5 1	
GCC CAG GTG GCA TTT ACA CCC TAC GCC CCG GAG CCC GGG AGC ACA TGC	207
Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys	
5 10 15	
CGG CTC AGA GAA TAC TAT GAC CAG ACA GCT CAG ATG TGC TGC AGC AAA	255
Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys	
20 25 30	
TGC TCG CCG GGC CAA CAT GCA AAA GTC TTC TGT ACC AAG ACC TCG GAC	303
Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp	
35 40 45 50	
ACC GTG TGT GAC TCC TGT GAG GAC AGC ACA TAC ACC CAG CTC TGG AAC	351
Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn	
55 60 65	
TGG GTT CCC GAG TGC TTG AGC TGT GGC TCC CGC TGT AGC TCT GAC CAG	399
Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln	
70 75 80	
GTG GAA ACT CAA GCC TGC ACT CGG GAA CAG AAC CGC ATC TGC ACC TGC	447
Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys Thr Cys	
85 90 95	
AGG CCC GGC TGG TAC TGC GCG CTG AGC AAG CAG GAG GGG TGC CGG CTG	495
Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys Arg Leu	
100 105 110	
TGC GCG CCG CTG CGC AAG TGC CGC CCG GGC TTC GGC GTG GCC AGA CCA	543
Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala Arg Pro	
115 120 125 130	
GGA ACT GAA ACA TCA GAC GTG GTG TGC AAG CCC TGT GCC CCG GGG ACG	591
Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro Gly Thr	
135 140 145	

TTC	TCC	AAC	ACG	ACT	TCA	TCC	ACG	GAT	ATT	TGC	AGG	CCC	CAC	CAG	ATC	639
Phe	Ser	Asn	Thr	Thr	Ser	Ser	Thr	Asp	Ile	Cys	Arg	Pro	His	Gln	Ile	
			150					155					160			
TGT	AAC	GTG	GTG	GCC	ATC	CCT	GGG	AAT	GCA	AGC	ATG	GAT	GCA	GTC	TGC	687
Cys	Asn	Val	Val	Ala	Ile	Pro	Gly	Asn	Ala	Ser	Met	Asp	Ala	Val	Cys	
		165					170					175				
ACG	TCC	ACG	TCC	CCC	ACC	CGG	AGT	ATG	GCC	CCA	GGG	GCA	GTA	CAC	TTA	735
Thr	Ser	Thr	Ser	Pro	Thr	Arg	Ser	Met	Ala	Pro	Gly	Ala	Val	His	Leu	
	180					185					190					
CCC	CAG	CCA	GTG	TCC	ACA	CGA	TCC	CAA	CAC	ACG	CAG	CCA	ACT	CCA	GAA	783
Pro	Gln	Pro	Val	Ser	Thr	Arg	Ser	Gln	His	Thr	Gln	Pro	Thr	Pro	Glu	
195					200					205					210	
CCC	AGC	ACT	GCT	CCA	AGC	ACC	TCC	TTC	CTG	CTC	CCA	ATG	GGC	CCC	AGC	831
Pro	Ser	Thr	Ala	Pro	Ser	Thr	Ser	Phe	Leu	Leu	Pro	Met	Gly	Pro	Ser	
			215					220					225			
CCC	CCA	GCT	GAA	GGG	AGC	ACT	GGC	GAC	TTC	GCT	CTT	CCA	GTT	GGA	CTG	879
Pro	Pro	Ala	Glu	Gly	Ser	Thr	Gly	Asp	Phe	Ala	Leu	Pro	Val	Gly	Leu	
			230				235						240			
ATT	GTG	GGT	GTG	ACA	GCC	TTG	GGT	CTA	CTA	ATA	ATA	GGA	GTG	GTG	AAC	927
Ile	Val	Gly	Val	Thr	Ala	Leu	Gly	Leu	Leu	Ile	Ile	Gly	Val	Val	Asn	
		245					250					255				
TGT	GTC	ATC	ATG	ACC	CAG	GTG	AAA	AAG	AAG	CCC	TTG	TGC	CTG	CAG	AGA	975
Cys	Val	Ile	Met	Thr	Gln	Val	Lys	Lys	Lys	Pro	Leu	Cys	Leu	Gln	Arg	
	260					265					270					
GAA	GCC	AAG	GTG	CCT	CAC	TTG	CCT	GCC	GAT	AAG	GCC	CGG	GGT	ACA	CAG	1023
Glu	Ala	Lys	Val	Pro	His	Leu	Pro	Ala	Asp	Lys	Ala	Arg	Gly	Thr	Gln	
275					280				285						290	
GGC	CCC	GAG	CAG	CAG	CAC	CTG	CTG	ATC	ACA	GCG	CCG	AGC	TCC	AGC	AGC	1071
Gly	Pro	Glu	Gln	Gln	His	Leu	Leu	Ile	Thr	Ala	Pro	Ser	Ser	Ser	Ser	
			295					300					305			
AGC	TCC	CTG	GAG	AGC	TCG	GCC	AGT	GCG	TTG	GAC	AGA	AGG	GCG	CCC	ACT	1119
Ser	Ser	Leu	Glu	Ser	Ser	Ala	Ser	Ala	Leu	Asp	Arg	Arg	Ala	Pro	Thr	
			310				315						320			
CGG	AAC	CAG	CCA	CAG	GCA	CCA	GGC	GTG	GAG	GCC	AGT	GGG	GCC	GGG	GAG	1167
Arg	Asn	Gln	Pro	Gln	Ala	Pro	Gly	Val	Glu	Ala	Ser	Gly	Ala	Gly	Glu	
		325					330					335				
GCC	CGG	GCC	AGC	ACC	GGG	AGC	TCA	GAT	TCT	TCC	CCT	GGT	GGC	CAT	GGG	1215
Ala	Arg	Ala	Ser	Thr	Gly	Ser	Ser	Asp	Ser	Ser	Pro	Gly	Gly	His	Gly	
	340				345						350					
ACC	CAG	GTC	AAT	GTC	ACC	TGC	ATC	GTG	AAC	GTC	TGT	AGC	AGC	TCT	GAC	1263
Thr	Gln	Val	Asn	Val	Thr	Cys	Ile	Val	Asn	Val	Cys	Ser	Ser	Ser	Asp	
355					360					365					370	

CAC	AGC	TCA	CAG	TGC	TCC	TCC	CAA	GCC	AGC	TCC	ACA	ATG	GGA	GAC	ACA	1311
His	Ser	Ser	Gln	Cys	Ser	Ser	Gln	Ala	Ser	Ser	Thr	Met	Gly	Asp	Thr	
				375					380					385		
GAT	TCC	AGC	CCC	TCG	GAG	TCC	CCG	AAG	GAC	GAG	CAG	GTC	CCC	TTC	TCC	1359
Asp	Ser	Ser	Pro	Ser	Glu	Ser	Pro	Lys	Asp	Glu	Gln	Val	Pro	Phe	Ser	
			390					395					400			
AAG	GAG	GAA	TGT	GCC	TTT	CGG	TCA	CAG	CTG	GAG	ACG	CCA	GAG	ACC	CTG	1407
Lys	Glu	Glu	Cys	Ala	Phe	Arg	Ser	Gln	Leu	Glu	Thr	Pro	Glu	Thr	Leu	
			405				410					415				
CTG	GGG	AGC	ACC	GAA	GAG	AAG	CCC	CTG	CCC	CTT	GGA	GTG	CCT	GAT	GCT	1455
Leu	Gly	Ser	Thr	Glu	Glu	Lys	Pro	Leu	Pro	Leu	Gly	Val	Pro	Asp	Ala	
	420					425					430					
GGG	ATG	AAG	CCC	AGT	TAACCAGGCC	GGTGTGGGCT	GTGTCGTAGC	CAAGGTGGGC								1510
Gly	Met	Lys	Pro	Ser												
435					440											
TGAGCCCTGG	CAGGATGACC	CTGCGAAGGG	GCCCTGGTCC	TTCCAGGCCC	CCACCACTAG											1570
GACTCTGAGG	CTCTTTCTGG	GCCAAGTTCC	TCTAGTGCCC	TCCACAGCCG	CAGCCTCCCT											1630
CTGACCTGCA	G															1641

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ala	Pro	Val	Ala	Val	Trp	Ala	Ala	Leu	Ala	Val	Gly	Leu	Glu	Leu	
-22		-20				-15						-10				
Trp	Ala	Ala	Ala	His	Ala	Leu	Pro	Ala	Gln	Val	Ala	Phe	Thr	Pro	Tyr	
-5						1				5					10	
Ala	Pro	Glu	Pro	Gly	Ser	Thr	Cys	Arg	Leu	Arg	Glu	Tyr	Tyr	Asp	Gln	
				15					20					25		
Thr	Ala	Gln	Met	Cys	Cys	Ser	Lys	Cys	Ser	Pro	Gly	Gln	His	Ala	Lys	
			30					35					40			
Val	Phe	Cys	Thr	Lys	Thr	Ser	Asp	Thr	Val	Cys	Asp	Ser	Cys	Glu	Asp	
		45					50					55				
Ser	Thr	Tyr	Thr	Gln	Leu	Trp	Asn	Trp	Val	Pro	Glu	Cys	Leu	Ser	Cys	
60						65					70					

Gly	Ser	Arg	Cys	Ser	Ser	Asp	Gln	Val	Glu	Thr	Gln	Ala	Cys	Thr	Arg	75	80	85	90
Glu	Gln	Asn	Arg	Ile	Cys	Thr	Cys	Arg	Pro	Gly	Trp	Tyr	Cys	Ala	Leu	95	100	105	
Ser	Lys	Gln	Glu	Gly	Cys	Arg	Leu	Cys	Ala	Pro	Leu	Arg	Lys	Cys	Arg	110	115	120	
Pro	Gly	Phe	Gly	Val	Ala	Arg	Pro	Gly	Thr	Glu	Thr	Ser	Asp	Val	Val	125	130	135	
Cys	Lys	Pro	Cys	Ala	Pro	Gly	Thr	Phe	Ser	Asn	Thr	Thr	Ser	Ser	Thr	140	145	150	
Asp	Ile	Cys	Arg	Pro	His	Gln	Ile	Cys	Asn	Val	Val	Ala	Ile	Pro	Gly	155	160	165	170
Asn	Ala	Ser	Met	Asp	Ala	Val	Cys	Thr	Ser	Thr	Ser	Pro	Thr	Arg	Ser	175	180	185	
Met	Ala	Pro	Gly	Ala	Val	His	Leu	Pro	Gln	Pro	Val	Ser	Thr	Arg	Ser	190	195	200	
Gln	His	Thr	Gln	Pro	Thr	Pro	Glu	Pro	Ser	Thr	Ala	Pro	Ser	Thr	Ser	205	210	215	
Phe	Leu	Leu	Pro	Met	Gly	Pro	Ser	Pro	Pro	Ala	Glu	Gly	Ser	Thr	Gly	220	225	230	
Asp	Phe	Ala	Leu	Pro	Val	Gly	Leu	Ile	Val	Gly	Val	Thr	Ala	Leu	Gly	235	240	245	250
Leu	Leu	Ile	Ile	Gly	Val	Val	Asn	Cys	Val	Ile	Met	Thr	Gln	Val	Lys	255	260	265	
Lys	Lys	Pro	Leu	Cys	Leu	Gln	Arg	Glu	Ala	Lys	Val	Pro	His	Leu	Pro	270	275	280	
Ala	Asp	Lys	Ala	Arg	Gly	Thr	Gln	Gly	Pro	Glu	Gln	Gln	His	Leu	Leu	285	290	295	
Ile	Thr	Ala	Pro	Ser	Ser	Ser	Ser	Ser	Ser	Leu	Glu	Ser	Ser	Ala	Ser	300	305	310	
Ala	Leu	Asp	Arg	Arg	Ala	Pro	Thr	Arg	Asn	Gln	Pro	Gln	Ala	Pro	Gly	315	320	325	330
Val	Glu	Ala	Ser	Gly	Ala	Gly	Glu	Ala	Arg	Ala	Ser	Thr	Gly	Ser	Ser	335	340	345	
Asp	Ser	Ser	Pro	Gly	Gly	His	Gly	Thr	Gln	Val	Asn	Val	Thr	Cys	Ile	350	355	360	

Val Asn Val Cys Ser Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln
365 370 375

Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro
380 385 390

Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser
395 400 405 410

Gln Leu Glu Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro
415 420 425

Leu Pro Leu Gly Val Pro Asp Ala Gly Met Lys Pro Ser
430 435

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3813 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: mouse
 - (B) STRAIN: C57BL/6
 - (G) CELL TYPE: T-helper cell
 - (H) CELL LINE: 7B9
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: 11
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 55..1479
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 121..1476
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: 55..120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGCAGCTGAG	GCACTAGAGC	TCCAGGCACA	AGGGCGGGAG	CCACCGCTGC	CCCT	ATG	57
						Met	
						-22	
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Ala Pro Ala Ala Leu Trp Val Ala Leu Val Phe Glu Leu Gln Leu Trp							
-20 -15 -10							
GCC ACC GGG CAC ACA GTG CCC GCC CAG GTT GTC TTG ACA CCC TAC AAA	153						
Ala Thr Gly His Thr Val Pro Ala Gln Val Val Leu Thr Pro Tyr Lys							
-5 1 5 10							
CCG GAA CCT GGG TAC GAG TGC CAG ATC TCA CAG GAA TAC TAT GAC AGG	201						
Pro Glu Pro Gly Tyr Glu Cys Gln Ile Ser Gln Glu Tyr Tyr Asp Arg							
15 20 25							
AAG GCT CAG ATG TGC TGT GCT AAG TGT CCT CCT GGC CAA TAT GTG AAA	249						
Lys Ala Gln Met Cys Cys Ala Lys Cys Pro Pro Gly Gln Tyr Val Lys							
30 35 40							
CAT TTC TGC AAC AAG ACC TCG GAC ACC GTG TGT GCG GAC TGT GAG GCA	297						
His Phe Cys Asn Lys Thr Ser Asp Thr Val Cys Ala Asp Cys Glu Ala							
45 50 55							
AGC ATG TAT ACC CAG GTC TGG AAC CAG TTT CGT ACA TGT TTG AGC TGC	345						
Ser Met Tyr Thr Gln Val Trp Asn Gln Phe Arg Thr Cys Leu Ser Cys							
60 65 70 75							
AGT TCT TCC TGT ACC ACT GAC CAG GTG GAG ATC CGC GCC TGC ACT AAA	393						
Ser Ser Ser Cys Thr Thr Asp Gln Val Glu Ile Arg Ala Cys Thr Lys							
80 85 90							
CAG CAG AAC CGA GTG TGT GCT TGC GAA GCT GGC AGG TAC TGC GCC TTG	441						
Gln Gln Asn Arg Val Cys Ala Cys Glu Ala Gly Arg Tyr Cys Ala Leu							
95 100 105							
AAA ACC CAT TCT GGC AGC TGT CGA CAG TGC ATG AGG CTG AGC AAG TGC	489						
Lys Thr His Ser Gly Ser Cys Arg Gln Cys Met Arg Leu Ser Lys Cys							
110 115 120							
GGC CCT GGC TTC GGA GTG GCC AGT TCA AGA GCC CCA AAT GGA AAT GTG	537						
Gly Pro Gly Phe Gly Val Ala Ser Ser Arg Ala Pro Asn Gly Asn Val							
125 130 135							
CTA TGC AAG GCC TGT GCC CCA GGG ACG TTC TCT GAC ACC ACA TCA TCC	585						
Leu Cys Lys Ala Cys Ala Pro Gly Thr Phe Ser Asp Thr Thr Ser Ser							
140 145 150 155							
ACT GAT GTG TGC AGG CCC CAC CGC ATC TGT AGC ATC CTG GCT ATT CCC	633						
Thr Asp Val Cys Arg Pro His Arg Ile Cys Ser Ile Leu Ala Ile Pro							
160 165 170							

GGA Gly	AAT Asn	GCA Ala	AGC Ser 175	ACA Thr	GAT Asp	GCA Ala	GTC Val	TGT Cys 180	GCG Ala	CCC Pro	GAG Glu	TCC Ser	CCA Pro 185	ACT Thr	CTA Leu	681
AGT Ser	GCC Ala	ATC Ile 190	CCA Pro	AGG Arg	ACA Thr	CTC Leu	TAC Tyr 195	GTA Val	TCT Ser	CAG Gln	CCA Pro	GAG Glu 200	CCC Pro	ACA Thr	AGA Arg	729
TCC Ser	CAA Gln 205	CCC Pro	CTG Leu	GAT Asp	CAA Gln	GAG Glu 210	CCA Pro	GGG Gly	CCC Pro	AGC Ser	CAA Gln 215	ACT Thr	CCA Pro	AGC Ser	ATC Ile	777
CTT Leu 220	ACA Thr	TCG Ser	TTG Leu	GGT Gly 225	TCA Ser 225	ACC Thr	CCC Pro	ATT Ile	ATT Ile	GAA Glu 230	CAA Gln	AGT Ser	ACC Thr	AAG Lys	GGT Gly 235	825
GGC Gly	ATC Ile	TCT Ser	CTT Leu	CCA Pro 240	ATT Ile	GGT Gly	CTG Leu	ATT Ile	GTT Val 245	GGA Gly	GTG Val	ACA Thr	TCA Ser	CTG Leu 250	GGT Gly	873
CTG Leu	CTG Leu	ATG Met	TTA Leu 255	GGA Gly	CTG Leu	GTG Val	AAC Asn 260	TGC Cys	ATC Ile	ATC Ile	CTG Leu	GTG Val	CAG Gln 265	AGG Arg	AAA Lys	921
AAG Lys	AAG Lys	CCC Pro 270	TCC Ser	TGC Cys	CTA Leu	CAA Gln	AGA Arg 275	GAT Asp	GCC Ala	AAG Lys	GTG Val 280	CCT Pro	CAT His	GTG Val	CCT Pro	969
GAT Asp 285	GAG Glu	AAA Lys	TCC Ser	CAG Gln	GAT Asp	GCA Ala 290	GTA Val	GGC Gly	CTT Leu	GAG Glu	CAG Gln 295	CAG Gln	CAC His	CTG Leu	TTG Leu	1017
ACC Thr 300	ACA Thr	GCA Ala	CCC Pro	AGT Ser	TCC Ser 305	AGC Ser	AGC Ser	AGC Ser	TCC Ser	CTA Leu 310	GAG Glu	AGC Ser	TCA Ser	GCC Ala	AGC Ser 315	1065
GCT Ala	GGG Gly	GAC Asp	CGA Arg 320	AGG Arg	GCG Ala	CCC Pro	CCT Pro	GGG Gly	GGC Gly 325	CAT His	CCC Pro	CAA Gln	GCA Ala	AGA Arg 330	GTC Val	1113
ATG Met	GCG Ala	GAG Glu	GCC Ala 335	CAA Gln	GGG Gly	TTT Phe	CAG Gln	GAG Glu 340	GCC Ala	CGT Arg	GCC Ala	AGC Ser 345	TCC Ser	AGG Arg	ATT Ile	1161
TCA Ser	GAT Asp 350	TCT Ser	TCC Ser	CAC His	GGA Gly	AGC Ser	CAC His 355	GGG Gly	ACC Thr	CAC His	GTC Val 360	AAC Asn	GTC Val	ACC Thr	TGC Cys	1209
ATC Ile 365	GTG Val	AAC Asn	GTC Val	TGT Cys	AGC Ser	AGC Ser 370	TCT Ser	GAC Asp	CAC His	AGT Ser	TCT Ser 375	CAG Gln	TGC Cys	TCT Ser	TCC Ser	1257
CAA Gln 380	GCC Ala	AGC Ser	GCC Ala	ACA Thr	GTG Val 385	GGA Gly	GAC Asp	CCA Pro	GAT Asp	GCC Ala 390	AAG Lys	CCC Pro	TCA Ser	GCG Ala	TCC Ser 395	1305

CCA AAG GAT GAG CAG GTC CCC TTC TCT CAG GAG GAG TGT CCG TCT CAG	1353
Pro Lys Asp Glu Gln Val Pro Phe Ser Gln Glu Glu Cys Pro Ser Gln	
400 405 410	
TCC CCG TGT GAG ACT ACA GAG ACA CTG CAG AGC CAT GAG AAG CCC TTG	1401
Ser Pro Cys Glu Thr Thr Glu Thr Leu Gln Ser His Glu Lys Pro Leu	
415 420 425	
CCC CTT GGT GTG CCG GAT ATG GGC ATG AAG CCC AGC CAA GCT GGC TGG	1449
Pro Leu Gly Val Pro Asp Met Gly Met Lys Pro Ser Gln Ala Gly Trp	
430 435 440	
TTT GAT CAG ATT GCA GTC AAA GTG GCC TGACCCCTGA CAGGGGTAAC	1496
Phe Asp Gln Ile Ala Val Lys Val Ala	
445 450	
ACCCTGCAAA GGGACCCCCG AGACCCTGAA CCCATGGAAC TTCATGACTT TTGCTGGATC	1556
CATTTCCCTT AGTGGCTTCC AGAGCCCCAG TTGCAGGTCA AGTGAGGGCT GAGACAGCTA	1616
GAGTGGTCAA AAACTGCCAT GGTGTTTTAT GGGGGCAGTC CCAGGAAGTT GTTGCTCTTC	1676
CATGACCCCT CTGGATCTCC TGGGCTCTTG CCTGATTCTT GCTTCTGAGA GGCCCCAGTA	1736
TTTTTTCCTT CTAAGGAGCT AACATCCTCT TCCATGAATA GCACAGCTCT TCAGCCTGAA	1796
TGCTGACACT GCAGGGCGGT TCCAGCAAGT AGGAGCAAGT GGTGGCCTGG TAGGGCACAG	1856
AGGCCCTTCA GGTTAGTGCT AAATCTTAG GAAGTACCCT CTCCAAGCCC ACCGAAATTC	1916
TTTTGATGCA AGAATCAGAG GCCCCATCAG GCAGAGTTGC TCTGTTATAG GATGGTAGGG	1976
CTGTAACTCA GTGGTCCAGT GTGCTTTTAG CATGCCCTGG GTTTGATCCT CAGCAACACA	2036
TGCAAAACGT AAGTAGACAG CAGACAGCAG ACAGCACAGC CAGCCCCCTG TGTGGTTTGC	2096
AGCCTCTGCC TTTGACTTTT ACTCTGGTGG GCACACAGAG GGCTGGAGCT CCTCCTCCTG	2156
ACCTTCTAAT GAGCCCTTCC AAGGCCACGC CTTCCCTCAG GGAATCTCAG GGAATCTCAG	2216
GTTCCCAGGC CCCTGCAGCC ACCTGTCTCT TCCTACCTCA GCCTGGAGCA CTCCCTCTAA	2276
CTCCCCAACG GCTTGGTACT GTACTTGCTG TGACCCCAAC GTGCATTGTC CGGGTTAGGC	2336
ACTGTGAGTT GGAACAGCTC ATGACATCGG TTGAAAGGCC CACCCGGAAA CAGCTAAGCC	2396
AGCTCTTTTG CCAAAGGATT CATGCCGGTT TTCTAATCAA CCTGCTCCCT AGCATTCGCT	2456
GGAAGGAAAG GGTTCAGGAG ACTCCTCAAG AAGCAAGTTC AGTCTCAGGT GCTTGGATGC	2516
CATGCTCACC GATTCCACTG GATATGAACT TGGCAGAGGA GCCTAGTTGT TGCCATGGAG	2576
ACTTAAAGAG CTCAGCACTC TGGAATCAAG ATACTGGACA CTTGGGGCCG ACTTGTTAAG	2636
GCTCTGCAGC ATCAGACTGT AGAGGGGAAG GAACACGTCT GCCCCCTGGT GGCCCGTCCT	2696

GGGATGACCT	CGGGCCTCCT	AGGCAACAAA	AGAATGAATT	GGAAAGGATG	TTCCTGGGTG	2756
TGGCCTAGCT	CCTGTGCTTG	TGTGGATCCC	TAAAGGGTGT	GCTAAGGAGC	AATTGCACTG	2816
TGTGCTGGAC	AGAATTCCTG	CTTATAAATG	CTTTTGTGTG	TTGTTTGTGA	CACTGAGCCC	2876
TGGCTGAGCC	ACCCACCCCC	ACCTCCCATC	CCACCTTTAC	ACGCCACTCT	TGCATGAGAA	2936
CCTGGCTGTC	TCCCACCTTG	AGCCTGTGGA	TGCTGAGGAA	ACACCCAGCC	AAGTAGACTC	2996
CAGGCTTGCC	CCTATCTCCT	GCTATGAGTC	TGGCCTCCTC	ATTGTGTTGT	GGGAAGGAGA	3056
CGGGTTCTGT	CATCTCGGAA	CGCCACACCC	GTGGATGTGA	ACAATGGCTG	TACTAGCTTA	3116
GACCAGCTTA	GGGCTCTGCA	TATCACAGGA	GGGGGAGCAG	GGAACAATTT	GAGTGCTGAC	3176
CTATAACACA	GTTCTTAAAG	GATCGGGCAG	TCCAGAATCT	CCTCCTTCAG	TGTGTGTGTG	3236
TGTGTGTGTG	TGTGTGTGTG	TGTGTGTGTG	TGTCCATGTT	TGCATGTATG	TGTGTGCCAG	3296
TGTGTGGAGG	CCCGAGGTTG	GCTTTGGGTG	TGTTTGATCA	CTCTCCAGTT	ACTGAGGCGG	3356
GCTCTCATCT	GTACCCAGAG	CTTGACATT	TTCTAGTCTA	ACTTGATTCA	GGGATCTCTG	3416
TCTGCCTATG	GAGGTGCTCA	GGTTACAGGC	AGGCTGCCAT	ACCTGCCCCG	CATTTACATG	3476
AATACTAGAG	ATCTGAATTC	TGGTCCTCAC	ACTTGTATAC	CTGCATTTTA	TCCACTAAGA	3536
CATCTCTCCA	AGGGCTCCCC	CTTCCTATTT	AATAAGTTAG	TTTTGAACTG	GCAAGATGGC	3596
TCAGTGGGTA	AGGCAGTTTG	CGGACAAACC	TGATGACCTG	AGTTGGATCC	CTGACCATAA	3656
GGTAGAAGAG	ACCTGATTCC	TGCAAGTTGT	CCTCTGACCA	CCACCCCAT	CATGCTTCTG	3716
CATATGTGCA	CACATCACAT	TCTTGCACAC	ACACTCACAT	ACCATAAATG	TAATAAATTT	3776
TTTTAAATAA	ATTGATTTTA	TCTTTTAAAA	AAAAAAA			3813

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Ala	Pro	Ala	Ala	Leu	Trp	Val	Ala	Leu	Val	Phe	Glu	Leu	Gln	Leu
-22		-20				-15						-10			
Trp	Ala	Thr	Gly	His	Thr	Val	Pro	Ala	Gln	Val	Val	Leu	Thr	Pro	Tyr
-5						1				5					10

Lys	Pro	Glu	Pro	Gly	Tyr	Glu	Cys	Gln	Ile	Ser	Gln	Glu	Tyr	Tyr	Asp	
				15					20						25	
Arg	Lys	Ala	Gln	Met	Cys	Cys	Ala	Lys	Cys	Pro	Pro	Gly	Gln	Tyr	Val	
			30					35					40			
Lys	His	Phe	Cys	Asn	Lys	Thr	Ser	Asp	Thr	Val	Cys	Ala	Asp	Cys	Glu	
		45					50					55				
Ala	Ser	Met	Tyr	Thr	Gln	Val	Trp	Asn	Gln	Phe	Arg	Thr	Cys	Leu	Ser	
	60					65					70					
Cys	Ser	Ser	Ser	Cys	Thr	Thr	Asp	Gln	Val	Glu	Ile	Arg	Ala	Cys	Thr	
75					80					85					90	
Lys	Gln	Gln	Asn	Arg	Val	Cys	Ala	Cys	Glu	Ala	Gly	Arg	Tyr	Cys	Ala	
				95					100					105		
Leu	Lys	Thr	His	Ser	Gly	Ser	Cys	Arg	Gln	Cys	Met	Arg	Leu	Ser	Lys	
			110					115					120			
Cys	Gly	Pro	Gly	Phe	Gly	Val	Ala	Ser	Ser	Arg	Ala	Pro	Asn	Gly	Asn	
		125					130					135				
Val	Leu	Cys	Lys	Ala	Cys	Ala	Pro	Gly	Thr	Phe	Ser	Asp	Thr	Thr	Ser	
	140					145					150					
Ser	Thr	Asp	Val	Cys	Arg	Pro	His	Arg	Ile	Cys	Ser	Ile	Leu	Ala	Ile	
155					160					165					170	
Pro	Gly	Asn	Ala	Ser	Thr	Asp	Ala	Val	Cys	Ala	Pro	Glu	Ser	Pro	Thr	
				175					180					185		
Leu	Ser	Ala	Ile	Pro	Arg	Thr	Leu	Tyr	Val	Ser	Gln	Pro	Glu	Pro	Thr	
			190					195					200			
Arg	Ser	Gln	Pro	Leu	Asp	Gln	Glu	Pro	Gly	Pro	Ser	Gln	Thr	Pro	Ser	
		205					210					215				
Ile	Leu	Thr	Ser	Leu	Gly	Ser	Thr	Pro	Ile	Ile	Glu	Gln	Ser	Thr	Lys	
	220					225					230					
Gly	Gly	Ile	Ser	Leu	Pro	Ile	Gly	Leu	Ile	Val	Gly	Val	Thr	Ser	Leu	
235					240					245					250	
Gly	Leu	Leu	Met	Leu	Gly	Leu	Val	Asn	Cys	Ile	Ile	Leu	Val	Gln	Arg	
				255					260					265		
Lys	Lys	Lys	Pro	Ser	Cys	Leu	Gln	Arg	Asp	Ala	Lys	Val	Pro	His	Val	
			270					275					280			
Pro	Asp	Glu	Lys	Ser	Gln	Asp	Ala	Val	Gly	Leu	Glu	Gln	Gln	His	Leu	
		285					290					295				

Leu	Thr	Thr	Ala	Pro	Ser	Ser	Ser	Ser	Ser	Ser	Leu	Glu	Ser	Ser	Ala
300						305					310				
Ser	Ala	Gly	Asp	Arg	Arg	Ala	Pro	Pro	Gly	Gly	His	Pro	Gln	Ala	Arg
315					320					325					330
Val	Met	Ala	Glu	Ala	Gln	Gly	Phe	Gln	Glu	Ala	Arg	Ala	Ser	Ser	Arg
				335					340					345	
Ile	Ser	Asp	Ser	Ser	His	Gly	Ser	His	Gly	Thr	His	Val	Asn	Val	Thr
			350					355					360		
Cys	Ile	Val	Asn	Val	Cys	Ser	Ser	Ser	Asp	His	Ser	Ser	Gln	Cys	Ser
		365					370					375			
Ser	Gln	Ala	Ser	Ala	Thr	Val	Gly	Asp	Pro	Asp	Ala	Lys	Pro	Ser	Ala
		380				385					390				
Ser	Pro	Lys	Asp	Glu	Gln	Val	Pro	Phe	Ser	Gln	Glu	Glu	Cys	Pro	Ser
395					400					405					410
Gln	Ser	Pro	Cys	Glu	Thr	Thr	Glu	Thr	Leu	Gln	Ser	His	Glu	Lys	Pro
				415					420					425	
Leu	Pro	Leu	Gly	Val	Pro	Asp	Met	Gly	Met	Lys	Pro	Ser	Gln	Ala	Gly
			430					435					440		
Trp	Phe	Asp	Gln	Ile	Ala	Val	Lys	Val	Ala						
		445					450								